

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/031,331C
Source: 1FW16
Date Processed by STIC: 12/21/04

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 12/21/2004
 PATENT APPLICATION: US/10/031,331C TIME: 14:42:39

Input Set : A:\yamada sequence listing.txt
 Output Set: N:\CRF4\12212004\J031331C.raw

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3 <110> APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
5 <120> TITLE OF INVENTION: Screening of genes to give tolerance against
6   environmental stress and the apprications
8 <130> FILE REFERENCE: YG12-12PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/031,331C
C--> 11 <141> CURRENT FILING DATE: 2002-01-18
13 <150> PRIOR APPLICATION NUMBER: JP P1999-235910
14 <151> PRIOR FILING DATE: 1999-07-19
16 <150> PRIOR APPLICATION NUMBER: JP P2000-85377
17 <151> PRIOR FILING DATE: 2000-03-24
19 <160> NUMBER OF SEQ ID NOS: 72
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1018
25 <212> TYPE: DNA
26 <213> ORGANISM: Bruguiera sexangula
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (42)..(464)
32 <400> SEQUENCE: 1
33 gtccaaacag ccagagagaa acgacaacat cgaccaagaa a atg gct ctt tca agc 56
34                                     Met Ala Leu Ser Ser
35                                     1           5
37 tct gct ctg aga acc gtc tct tct tct gtg aag gtg gtc ggc cct gca 104
38 Ser Ala Leu Arg Thr Val Ser Ser Ser Val Lys Val Val Gly Pro Ala
39           10           15           20
41 aga tca aag agt gct act gta ccc acc caa aca gta ttg cct ttc aag 152
42 Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr Val Leu Pro Phe Lys
43           25           30           35
45 ttc aca aac ccg tcg tta ctc act cga tcg cta agc ttt tca tca aaa 200
46 Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu Ser Phe Ser Ser Lys
47           40           45           50
49 ggt tca agc ttt gac agc ttc tct gta ccc aaa aga tct ttt tct tgc 248
50 Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys Arg Ser Phe Ser Cys
51           55           60           65
53 aga agc caa gcc act cca tct gat gat gcc tca aga ccc acc aaa gtt 296
54 Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser Arg Pro Thr Lys Val
55 70           75           80           85
57 caa gag ctg tgt gtg tat gag atg aac gag aga gat cgt gga agc cct 344
58 Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg Asp Arg Gly Ser Pro
59           90           95           100
61 gct gtt ctc cgg ttg agc cag aaa cct gtt aat tct ctc ggc gat ctc 392
62 Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn Ser Leu Gly Asp Leu

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63          105          110          115
65 gtg cct ttc agt aac aaa gtt tac agc gga gac ctg cag aag cga att 440
66 Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp Leu Gln Lys Arg Ile
67          120          125          130
69 gga gta acc gca gaa tat gca tcc tgatccaaaa caagccagaa aaaaaggggtg 494
70 Gly Val Thr Ala Glu Tyr Ala Ser
71          135          140
73 atcgctttga agcgatatat agctttttatt tcgggtggcta tggtcacatt gctgtgcaag 554
75 ggcatactt gacctacgag gacacgcacc ttgctgtgac gggcggggtcg ggcataatttg 614
77 aaggagtgtc tggtcaggtt aagctgcagc aactcgtgta ccctttcaag ctcttctaca 674
79 ctttctactt gcgaggcatc aaggacttgc cggaggagct tacgaagaag ccggttgagc 734
81 cccacccttc tgttgagccg atgccggcgg ccaaggcttg cgagccacat gccgttggtg 794
83 ctaatttcac cgattagtga ttaattgtcc ttttgggggtt cggatgaact tgagttagct 854
85 tacagttgca caacgttatg gcgcgagaca cgagagggaa ccttagccat aagaaaatta 914
87 ataatctcac ggtgctttta ttttgattct tctattagtt gaatcgttaa tgaaagtgga 974
89 ccaaattggc tgttttacgt tttaaaaaaa aaaaaaaaaa aaaa 1018
92 <210> SEQ ID NO: 2
93 <211> LENGTH: 141
94 <212> TYPE: PRT
95 <213> ORGANISM: Bruguiera sexangula
97 <400> SEQUENCE: 2
98 Met Ala Leu Ser Ser Ser Ala Leu Arg Thr Val Ser Ser Ser Val Lys
99 1          5          10          15
101 Val Val Gly Pro Ala Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr
102          20          25          30
104 Val Leu Pro Phe Lys Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu
105          35          40          45
107 Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys
108          50          55          60
110 Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser
111 65          70          75          80
113 Arg Pro Thr Lys Val Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg
114          85          90          95
116 Asp Arg Gly Ser Pro Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn
117          100          105          110
119 Ser Leu Gly Asp Leu Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp
120          115          120          125
122 Leu Gln Lys Arg Ile Gly Val Thr Ala Glu Tyr Ala Ser
123          130          135          140
127 <210> SEQ ID NO: 3
128 <211> LENGTH: 2060
129 <212> TYPE: DNA
130 <213> ORGANISM: Bruguiera sexangula
132 <220> FEATURE:
133 <221> NAME/KEY: CDS
134 <222> LOCATION: (81)..(1718)
136 <400> SEQUENCE: 3
137 cgaaattcct ctactaacia taccagatcc agtctagcgt ttcgattttc tgcttcacat 60
139 ttctgtttct ttgaccagaa atg gca atc gcg gct caa act ccg gac att ctc 113

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140           Met Ala Ile Ala Ala Gln Thr Pro Asp Ile Leu
141           1      5      10
143 ggc gaa cgt cag tcc ggc cag gac gtc cgc act caa aat gtg gtg gca 161
144 Gly Glu Arg Gln Ser Gly Gln Asp Val Arg Thr Gln Asn Val Val Ala
145           15      20      25
147 tgt caa gcg gtt gcc aat att gtc aaa tct tca ctt ggt cct gtc gga 209
148 Cys Gln Ala Val Ala Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly
149           30      35      40
151 ctc gac aag atg cta gtg gat gat att ggt gat gta aca att aca aat 257
152 Leu Asp Lys Met Leu Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn
153           45      50      55
155 gat ggt gct acg att ctt aag atg tta gaa gta gag cat cct gca gca 305
156 Asp Gly Ala Thr Ile Leu Lys Met Leu Glu Val Glu His Pro Ala Ala
157 60      65      70      75
159 aag gtg ctc gtg gag ttg gct gag ctt caa gac cga gaa gtt gga gat 353
160 Lys Val Leu Val Glu Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp
161           80      85      90
163 gga acc act tcg gtt gtc atc ata gca gct gag ttg ctc aag aga gca 401
164 Gly Thr Thr Ser Val Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala
165           95      100      105
167 aat gat ctc gtg agg aat aag atc cac cca aca tca ata atc agt gga 449
168 Asn Asp Leu Val Arg Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly
169           110      115      120
171 tac agg ctt gct atg agg gaa gca tgc aag tat gtt gaa gag aaa ttg 497
172 Tyr Arg Leu Ala Met Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu
173           125      130      135
175 tca atg aag gtt gaa aag ctt gga aaa gat tct cta gta aac tgt gca 545
176 Ser Met Lys Val Glu Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala
177 140      145      150      155
179 aag aca agc atg tcc tca aag ttg ata gct ggt gac agc gac ttc ttt 593
180 Lys Thr Ser Met Ser Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe
181           160      165      170
183 gca aat ttg gtt gta gat gct gta caa gca gta aag atg acc aat gca 641
184 Ala Asn Leu Val Val Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala
185           175      180      185
187 cgg ggg gaa atc aaa tat cct atc aag agt ata aat att ttg aaa gct 689
188 Arg Gly Glu Ile Lys Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala
189           190      195      200
191 cat gga aaa agt gca aga gat agc tgc ctt ttg aat ggc tat gct ctc 737
192 His Gly Lys Ser Ala Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu
193           205      210      215
195 aat act ggt cgt gct gct caa ggg atg cct atg aga gtt gca cct gca 785
196 Asn Thr Gly Arg Ala Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala
197 220      225      230      235
199 agg att gct tgt ctt gac ttt aat ctt cag aaa acg aag atg caa ttg 833
200 Arg Ile Ala Cys Leu Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu
201           240      245      250
203 ggt gta caa gtc tta gtc act gat ccc agg gag ctt gaa aga att cgt 881
204 Gly Val Gln Val Leu Val Thr Asp Pro Arg Glu Leu Glu Arg Ile Arg

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205	255	260	265	
207	caa aga gaa gct gat atg aca aag gaa cgg att gag aaa ctc ctg aaa	929		
208	Gln Arg Glu Ala Asp Met Thr Lys Glu Arg Ile Glu Lys Leu Leu Lys			
209	270 275 280			
211	gct gga gca aat gtt gtt cta acc aca aag gga att gat gac atg gca	977		
212	Ala Gly Ala Asn Val Val Leu Thr Thr Lys Gly Ile Asp Asp Met Ala			
213	285 290 295			
215	ctt aaa tat ttt gtg gag gct ggg gct att gct gtg aga cgt gtt cgg	1025		
216	Leu Lys Tyr Phe Val Glu Ala Gly Ala Ile Ala Val Arg Arg Val Arg			
217	300 305 310 315			
219	aaa gag gat atg cgc cat gtt gcc aag gca act ggt gca aca ctg gtt	1073		
220	Lys Glu Asp Met Arg His Val Ala Lys Ala Thr Gly Ala Thr Leu Val			
221	320 325 330			
223	tca aca ttt gct gac atg gaa gga gag gaa aca ttt gat tca tca ctg	1121		
224	Ser Thr Phe Ala Asp Met Glu Gly Glu Glu Thr Phe Asp Ser Ser Leu			
225	335 340 345			
227	ctt gga caa gct gaa gaa gtt gtg gag gag cgc att gct gat gac gat	1169		
228	Leu Gly Gln Ala Glu Glu Val Val Glu Glu Arg Ile Ala Asp Asp Asp			
229	350 355 360			
231	gtg att atg ata aaa ggg aca aag act aca agt gcg gtt tcc ttg att	1217		
232	Val Ile Met Ile Lys Gly Thr Lys Thr Thr Ser Ala Val Ser Leu Ile			
233	365 370 375			
235	ctt cgt ggt gca aat gac tat atg ctc gat gag atg gag cga gcc ctg	1265		
236	Leu Arg Gly Ala Asn Asp Tyr Met Leu Asp Glu Met Glu Arg Ala Leu			
237	380 385 390 395			
239	cat gat gct tta tgt att gtc aag aga acc ctt gaa tct aat aca gta	1313		
240	His Asp Ala Leu Cys Ile Val Lys Arg Thr Leu Glu Ser Asn Thr Val			
241	400 405 410			
243	gtt gca ggt gga ggt gct gtt gag gct gcc ttg tct gtg cac ttg gag	1361		
244	Val Ala Gly Gly Gly Ala Val Glu Ala Ala Leu Ser Val His Leu Glu			
245	415 420 425			
247	tac ctc gct aca act ctt ggg tca cga gag cag tta gca ata gca gag	1409		
248	Tyr Leu Ala Thr Thr Leu Gly Ser Arg Glu Gln Leu Ala Ile Ala Glu			
249	430 435 440			
251	ttt gca gaa tcc ttg ttg att ata cca aag gtt ctt gct gtc aat gct	1457		
252	Phe Ala Glu Ser Leu Leu Ile Ile Pro Lys Val Leu Ala Val Asn Ala			
253	445 450 455			
255	gcc aaa gat gcc act gaa tta gct gca aaa ctc cgg gct tac cac cat	1505		
256	Ala Lys Asp Ala Thr Glu Leu Ala Ala Lys Leu Arg Ala Tyr His His			
257	460 465 470 475			
259	aca gca caa aca aag gct gat aag aaa cat tta tca agc atg gga cta	1553		
260	Thr Ala Gln Thr Lys Ala Asp Lys Lys His Leu Ser Ser Met Gly Leu			
261	480 485 490			
263	gac ctt tca aag ggg acc atc cga aac aac tta gaa gct gga gtc att	1601		
264	Asp Leu Ser Lys Gly Thr Ile Arg Asn Asn Leu Glu Ala Gly Val Ile			
265	495 500 505			
267	gaa cct gca atg agc aaa ata aag ata att cag ttt gct act gaa gca	1649		
268	Glu Pro Ala Met Ser Lys Ile Lys Ile Ile Gln Phe Ala Thr Glu Ala			
269	510 515 520			

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271 gcc ata aca att ctt cga att gat gac atg atc aag ctt gtc aag gat      1697
272 Ala Ile Thr Ile Leu Arg Ile Asp Asp Met Ile Lys Leu Val Lys Asp
273      525                      530                      535
275 gag act cag aat gaa gag gaa tagatgcaga ctcttgtaag ctgcctccct      1748
276 Glu Thr Gln Asn Glu Glu Glu
277 540                      545
279 tttgtttttca aatttgtgtc ccttgcgagc tggaggaaag ggggggtgtt tatgtggtgt 1808
281 tttcagtggg ttttaattttt caaggagctc gcggcctgtg tacttttaggt tagagtcctat 1868
283 ccaaggggtg tttatttgat aatgcctaag ctgtttctcg tctattagta ggctggtagt 1928
285 tccactgagt tctcatccca attaaaagaa tgagatcaaa gggtcctaaa ttcgtactca 1988
287 ttggtgcacg atttgtttct gacaagcata agacttgacc ctctctatca caataaaaaa 2048
289 aaaaaaaaaa aa      2060
292 <210> SEQ ID NO: 4
293 <211> LENGTH: 546
294 <212> TYPE: PRT
295 <213> ORGANISM: Bruguiera sexangula
297 <400> SEQUENCE: 4
298 Met Ala Ile Ala Ala Gln Thr Pro Asp Ile Leu Gly Glu Arg Gln Ser
299      1                      5                      10                      15
301 Gly Gln Asp Val Arg Thr Gln Asn Val Val Ala Cys Gln Ala Val Ala
302      20                      25                      30
304 Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly Leu Asp Lys Met Leu
305      35                      40                      45
307 Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn Asp Gly Ala Thr Ile
308      50                      55                      60
310 Leu Lys Met Leu Glu Val Glu His Pro Ala Ala Lys Val Leu Val Glu
311      65                      70                      75                      80
313 Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp Gly Thr Thr Ser Val
314      85                      90                      95
316 Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala Asn Asp Leu Val Arg
317      100                     105                     110
319 Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly Tyr Arg Leu Ala Met
320      115                     120                     125
322 Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu Ser Met Lys Val Glu
323      130                     135                     140
325 Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala Lys Thr Ser Met Ser
326      145                     150                     155                     160
328 Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe Ala Asn Leu Val Val
329      165                     170                     175
331 Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala Arg Gly Glu Ile Lys
332      180                     185                     190
334 Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala His Gly Lys Ser Ala
335      195                     200                     205
337 Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu Asn Thr Gly Arg Ala
338      210                     215                     220
340 Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala Arg Ile Ala Cys Leu
341      225                     230                     235                     240
343 Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu Gly Val Gln Val Leu
344      245                     250                     255

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date